METHODS OF INHIBITING *HELICOBACTER PYLORI*

This invention relates to methods of screening molecules capable of inhibiting the survival of *Helicobacter*, particularly *Helicobacter pylori*, *in vivo* by specifically inhibiting the activity of UreI, to the molecules identified by these methods, and to the use of these molecules to treat or prevent *Helicobacter* infection.

BACKGROUND OF INVENTION

Helicobacter pylori is a microaerophilic Gram-negative bacterium, which colonizes the gastric mucosa of humans (10). *H. pylori* is associated with gastritis and peptic ulcer disease and has been shown to increase the risk of gastric cancers. Urease is a major virulence factor of *H. pylori*. It is involved in neutralizing the acidic microenvironment of the bacterium and also plays a role in *H. pylori* metabolism (11, 26).

The urease region of the *H. pylori* genome is composed of two gene clusters common to all strains (9 and Figure 1), one comprising the *ureAB* genes encoding the structural urease subunits and the other containing the *ureEFGH* genes encoding the accessory proteins required for nickel incorporation into the urease active site. The *ureI* gene lies immediately upstream from this latter gene cluster and is transcribed in the same direction (Figure 1). The *ureA*, *ureB*, ureE, ureF, *ureG*, *ureH*, and *ureI* genes and gene products have been described and claimed in United States Patent 5,695,931 and allowed patent application Serial No. 08/472,285, both of which are specifically incorporated herein by reference.

The distances separating *ureI* from *ureE* (one base pair, bp) and *ureE* from *ureF* (11 bp) suggest that *ureI-ureE-ureF* constitute an operon. Cotranscription of *ureI* and *ureE* has been demonstrated by northern blot analysis (1). An *H. pylori* N6 mutant with a *ureI* gene disrupted by a MiniTn*3*-Km transposon was previously described by Ferrero et al. (1994) (13). This strain (N6-*ureI*::TnKm-8) presented a urease negative phenotype, so it was concluded that *ureI* was an accessory gene required for full urease activity.

The sequences of UreI from *H. pylori* and the AmiS proteins, encoded by the aliphatic amidase operons of *Pseudomonas aeruginosa* and *Rhodococcus* sp. R312, are similar (5, 27). Aliphatic amidases catalyze the intracellular hydrolysis of short-chain aliphatic amides to produce the corresponding organic acid and ammonia. It has been shown

that *H. pylori* also has such an aliphatic amidase, which hydrolyzes acetamide and propionamide *in vitro* (23).

In view of the sequence similarity between UreI and AmiS together with the very similar structures of the urease and amidase substrates (urea: NH_2-CO-NH_2 and acetamide: CH_3-CO-NH_2) and the production of ammonia by both enzymes, a better understanding of the function of the *H. pylori* UreI protein is required. This understanding will open new opportunities for the prevention and treatment of *H. pylori* infections.

SUMMARY OF THE INVENTION

This invention provides methods for identifying molecules capable of inhibiting the growth and/or survival of *Helicobacter* species, particularly, *H. pylori*, *in vivo*. In particular, the methods of this invention involve screening molecules that specifically inhibit UreI protein function.

The invention encompasses the molecules identified by the methods of this invention and the use of the molecules by the methods of this invention to treat or prevent *Helicobacter*, and particularly *H. pylori*, infection in humans and animals.

Another aspect of this invention is a method of preventing or treating *Helicobacter* species infection by administration to a human or animal in need of such treatment a molecule capable of inhibiting the growth and/or survival of *Helicobacter* species *in vivo*. One such molecule according to the invention is characterized by a high affinity for UreI, which allows it (i) to be transported inside the *Helicobacter* cell, or (ii) to inhibit transport properties of UreI, or (iii) to inhibit UreI function by inhibiting UreI interaction with urease or other *Helicobacter* proteins. By inhibiting UreI, such molecule renders the bacteria more sensitive to acidity.

Yet another aspect of this invention is the production of immunogenic UreI antigens and their use as vaccines to prevent *Helicobacter* species infection and/or colonization of the stomach or the gut. Antibodies to these UreI antigens are also encompassed within the scope of this invention.

This invention further relates to recombinant strains of *H. pylori* comprising a modified *ureI* gene, such that the products of the modified gene contribute to the attenuation of the bacteria's ability to survive *in vivo*, and thus, its pathogenic effects.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 depicts the urease gene cluster of *H. pylori* parental strains N6 and SS1 and of the derived mutants deficient in UreI, strains N6-823, N6-834, and SS1-834. The genes are indicated by boxes with an arrow showing the direction of their transcription. The distances between the *ure* genes are given in base pairs, bp. The site hybridizing to the primers used to confirm correct allelic exchange in strains N6-823, N6-834, and SS1-834 is shown. Blank boxes represent the cassettes containing the genes conferring resistance to Cm (cat) or to Km (*aphA-3*). The urease activity of these strains is given on the right-hand side of the figure. Urease activity was measured as the release of ammonia on crude extracts of bacteria grown 48 hours on blood agar plates as described previously (9). One unit corresponds to the amount of enzyme required to hydrolyze 1 µmol of urea min^{-1} mg^{-1} total protein. The data are means ± standard deviation calculated from 3 to 5 determinations.

Figure 2A depicts a restriction map of pILL823, pILL824, pILL833 and pILL834. Small boxes mark the vector of each plasmid, and large boxes correspond to genes. *Ori* indicates the position of the ColE1 origin of replication. Sp^R and Ap^R are the genes conferring resistance to spectinomycin and ampicillin, respectively. Cassettes inserted into *ureI* and conferring resistance to chloramphenicol (*cat*) or kanamycin (*aphA-3*) are also shown. The sequence of the DNA region comprising the *ureI* stop codon and the *ureE* start codon, including the *BclI* site where adaptor H19 was inserted, is given. Insertion of H19 into the *BclI* site of pILL824 produced pILL825, the resulting *ureI-ureE* intergenic region is also shown. The stop codon of *ureI* and the start codon of *ureE* are boxed and the ribosome binding site (RBS) is underlined. Brackets indicate the position of restriction sites removed by ligation.

Figure 2B depicts a restriction map of two *H. pylori/E. coli* shuttle plasmids: pILL845 and pILL850. Small boxes mark the vector of each plasmid, and large boxes correspond to genes. *Ori* indicates the position of the *E. coli* ColE1 origin of replication and *repA* the gene coding for the RepA protein necessary for autonomous replication of the pHel2 in *H. pylori*. Cm^P marks the gene conferring resistance to chloramphenicol. The *ureI* promoter is represented by a "P" with an arrow indicating the direction of the transcription. The other symbols are as in Figure 1.

Figure 3 shows the alignment of the amino acid sequence of UreI from *H. pylori* with those of similar proteins and prediction of the two-dimensional structure of members of the UreI/AmiS protein family. Residues identical at one position in, at least, four sequences are boxed, and dashes indicate gaps inserted to optimize alignment. The organisms from which the sequences originated and the degree of identity with the *H. pylori* UreI protein are: UreI-Hp, *Helicobacter pylori* (195 residues, accession No. M84338); UreI-Hf, *Helicobacter felis* (74% identity over 196 residues, accession No. A41012); UreI-Lacto, *Lactobacillus fermentum* (55% identity over the 46 residues-long partial sequence, accession No. D10605); UreI-Strepto, *Streptococcus salivarius* (54% identity over the 129 residues-long partial sequence, accession No. U35248); AmiS-Myco, *Mycobacterium smegmatis* (39% identity over 172 residues, accession No. X57175); AmiS-Rhod, *Rhodococcus* sp. R312 (37% identity over 172 residues accession No. Z46523) and AmiS-Pseudo, *Pseudomonas aeruginosa* (37% identity over 171 residues, accession No. X77161). Predicted transmembrane ∀-helices are shown as shaded boxes. The regions separating these boxes are hydrophilic loops labeled "IN" when predicted to be intracellular and "OUT" when predicted to be extracellular.

Figure 4 depicts the kinetics of ammonium release by the N6 parental strain (panel A) and the UreI-deficient strain N6-834 (panel B). Bacteria ($2X10^8$/ml) were harvested and washed (as described in Skouloubris et al. (30)) resuspended in 10 ml of phosphate saline buffer (PBS) at pH 7, 5 or 2.2 in the presence of 10mM urea. After 0, 3, 5 and 30 minutes, 0.5ml were withdrawn and centrifuged to eliminate bacteria. The supernatant was kept on ice until ammonium concentration was measured using the assay commercialized by Sigma (kit reference #171).

Table 2 shows the results obtained with the *in vitro* viability tests and the pH measurements.

Table 3 gives the values of ammonium production by strain N6 and N6-834 presented on the graphs of Figure 4.

DETAILED DESCRIPTION

The urease cluster of *Helicobacter* species is unique among the many urease operons of Gram-negative bacteria that have been sequenced (20) in that it has an extra gene, ***ureI***.

The function of UreI has therefore been the subject of much speculation. It has mostly been attributed the function of an accessory protein required for nickel incorporation at the urease active site or a nickel transporter. A *H. pylori* strain carrying a deletion of *ureI* replaced by a non-polar cassette (Kanamycin resistance cassette) has been constructed and was named N6-834 (30). The strain has been deposited at C.N.C.M. (Collection Nationale de Culture de Microorganismes, 25 rue du Docteur Roux, 75724 Paris Cédex 15, France) on June 28, 1999. This is the first time that a non-polar cassette (19) has been shown to be functional in *H. pylori*. These results provide a valuable tool for genetic analysis of complex *H. pylori* operons, such as Cag, a multigenic pathogenicity island.

Studies with this strain demonstrated that UreI is not required for full activity of *H. pylori* urease as measured after *in vitro* growth at neutral pH. This result argues against UreI being involved in nickel transport since such a protein, NixA (3) already identified in *H. pylori*, is necessary for full urease activity. Comparing ureases expressed from a UreI-deficient strain and the corresponding parental strain show that (i) they present the same activity optimum pH (pH 8); (ii) the urease structural subunits, UreA-B, are produced in equal amounts; and (iii) the urease cellular location is identical.

It is demonstrated here that (i) UreI is essential for colonization of mice by *H. pylori*; (ii) UreI is important for survival of *H. pylori* at acidic pH; and (iii) UreI is necessary for urease "activation" at low pH.

H. pylori during the colonization process of the stomach has to deal with important pH variations and especially has to adapt rapidly to extremely acidic pH (as acidic as pH 1.4). We have shown that UreI is required for *H. pylori* adaptation to acidity, consistently with the absence of colonization of the mouse stomach. As an essential protein for the *H. pylori* resistance to acidity, UreI certainly plays a key role in the infection, establishment, and persistence of *H. pylori*. UreI has a sequence similar to those of the AmiS proteins, proposed to be involved in the transport of short-chain amides (27), molecules structurally similar to urea. The UreI/AmiS proteins have the characteristics of integral membrane proteins, probably of the cytoplasmic membrane.

Different roles for UreI can be proposed. For instance, UreI might be involved in transport (import or export) of urea or short chain amides specifically active at low pH. However, an essential role for UreI as an amide transporter is less likely because a SS1

mutant, deficient in aliphatic amidase, colonizes as efficiently as the parental strain in mouse colonization experiments. In addition, amidase activity is not significantly modified by the deletion of *ureI* in the X6-834 mutant strain (C.N.C.M. filed on June 28,1999). Import or export of urea could be consistent with the existence of a urea cycle, which is one of the characteristics of *H. pylori* (28).

Alternatively, UreI might be involved in an active ammonium export system. Finally, UreI might be involved in a mechanism of coupling urease activity to the periplasmic pH, allowing urease to become more active when extracellular pH is acidic.

Our results are compatible with the first hypothesis of UreI being an urea transporter active at acidic pH values and the third hypothesis of UreI being a kind of sensor protein between the periplasmic pH and urease activity. We think that these two hypothesis are not exclusive. Whatever the role of UreI, as a membrane protein essential for the survival of *H. pylori in vivo*, it now provides a powerful target for a new eradication therapy and for vaccines against *H. pylori*.

Molecules capable of inhibiting the growth and/or survival of *Helicobacter in vivo* may be identified by contacting a parental *Helicobacter* strain with said molecule in a biological sample; testing and comparing, in the presence or absence of urea, the sensitivity to the extracellular pH of the parental strain to a strain deficient in UreI and to a UreI deficient strain complemented with *ureI;* selecting said molecules displaying a differential effect on the parental or complemented strain as compared to the UreI deficient strain; and collecting said active molecule.

A molecule active specifically on UreI will be the one rendering *H. pylori* sensitive to acidic pH (pH 2.2) in the presence of urea without affecting the strain behavior at neutral pH. Sensitivity to acidity in the presence of urea can be tested on whole *H. pylori* cells following a protocol described in the examples and adapted from Clyne *et al.* (8). We are now trying to transpose this test in *E. coli* whole cells carrying the complete urease gene cluster on a plasmid (*ureAB-ureIEFGH*). Screening for a molecule rendering this recombinant *E. coli* more sensitive to acidity in the presence of urea will be performed as described for *H. pylori* in the examples. To distinguish between inhibitory molecules acting on UreI and those acting on urease, the medium pH after whole cell incubation at pH 7 in the presence of urea will be measured. Interesting molecules are those affecting response to

acidity without inhibiting the alkalization of the medium observed after incubation at neutral pH.

These methods may be used to identify molecules that inhibit any *Helicobacter* species carrying a UreI-homolog. This includes the gastric *Helicobacter* species: *Helicobacter pylori*, *Helicobacter felis*, *Helicobacter mustelae*, *Helicobacter muridarum*, and also *Helicobacter heilmannii*, *Helicobacter canis*, *Helicobacter bilis*, *Helicobacter hepaticus*, and *Helicobacter trogontum*.

The molecules identified by the methods of this invention will be capable of inhibiting UreI activity by (i) inhibiting transport of urea or short chain amides, (ii) inhibiting ammonium export, or (iii) inhibiting urease "activation" at low pH. The molecules according to point (i) and (ii) should be able to diffuse throughout the outer membrane and should be active even at low concentration. Suitable candidate molecules are structural analogs of urea or short chain amides, ammonium derivatives or urease inhibitors. For example, molecules derived from AHA (acetohydroxamic acid), hydroxyurea, hippuric acid, flurofamide, hydroxylamine, methylurea, thiourea (29), or methylammonium. The molecules according to point (iii) should inhibit the contact between UreI (probably inserted in the cytoplasmic membrane) and periplasmic, membrane, or cytoplasmic *H. pylori* proteins, which are necessary for urease "activation" at low pH. These proteins could be the structural subunits of urease itself, the accessory proteins, or other proteins. Molecules obtained according to this invention should not be urease competitive inhibitors, should not be toxic or mutagenic *in vivo* and could potentialize the action of antibiotics or bactericidal molecules. Validation of the action of such molecules could be performed *in vivo* in the mouse animal model with the pair of isogenic strains SS1 and SS1-834 as described in the examples.

One example of a molecule according to this invention is a monoclonal or polyclonal antibody specific for UreI. Preferably, the antibody is capable of specifically inhibiting UreI activity.

The molecules of this invention may be administered in combination with a pharmaceutically acceptable carrier to a patient suffering from a *Helicobacter* infection. Alternatively, immunogenic compositions comprising one or more molecules according to this invention may be administered in a vaccine composition to prevent infection by *Helicobacter* species.

Immunogenic compositions according to this invention may also comprise all or part of the UreI protein. Preferably, the UreI fragments comprise at least 10 consecutive amino acids of the native UreI sequence and more preferably, the fragments comprise at least 18, 20, or 25 consecutive amino acids of the native UreI sequence. Other suitable UreI fragments may contain at least 40 or at least 100 consecutive amino acids of the native UreI sequence. Suitable fragments of *Helicobacter pylori* include, for example, fragments selected from the group consisting of amino acid residues 22 to 31, 49 to 74, 94 to 104, and 123 to 142 of *H. pylori* (GenBank accession No. M84338)

Reference will now be made to the following Examples. The Examples are purely exemplary of the invention and are not to be construed as limiting of the invention.

EXAMPLES

Construction of defined mutations of the *H. pylori ureI* gene

H. pylori strains with defined mutations in *ureI* were generated by allelic exchange to determine whether the UreI protein was necessary for production of active urease. For this purpose, two plasmids (pILL823 and pILL834) with cassettes carrying antibiotic resistance genes inserted in *ureI* were constructed in *E. coli*.

In one plasmid, pILL823 (Figure 2A), the *ureI* gene was inactivated by insertion of a promoterless *cat* gene, conferring resistance to chloramphenicol (Cm). A 780 bp blunt-ended *Bam*HI restriction fragment containing the "cat cartridge" from pCM4 (Pharmacia, Sweden) was introduced into a unique *Hpa*I site, between codons 21 and 22 of *ureI*, in pILL753 (9). In the resulting plasmid, pILL823 (Figure 2A), *cat* is in the same orientation as *ureI* and is expressed under the control of the *ureI* promoter.

The second plasmid, pILL834, carried a *ureI* gene in which all but the first 21 codons were deleted and replaced with a non-polar cassette composed of the *aphA*-3 kanamycin (Km) resistance gene (25), which has been deleted from its own promoter and terminator regions (19). In *Shigella flexneri* (19) and other organisms (such as *Yersinia enterocolitica*, 2) this cassette has been shown not to affect the transcription of the genes downstream within an operon as long as these distal genes have intact translation signals. There is only one base pair separating *ureI* from *ureE* (Figure 1) and *ureE* does not have an RBS (ribosome binding site) of its own, so the expression of *ureI* and *ureE* is

transcriptionally and translationally coupled. Therefore, a *ureI* deletion was accompanied by the addition of an RBS immediately upstream from *ureE*. Three intermediates, pILL824, pILL825 and pILL833 (Figure 2A), were constructed in order to produce the final plasmid, pILL834 (Figure 2A). A 1.8 Kb *Hpa*I-*Hin*dIII restriction fragment from pILL753 (9) was inserted between the *Eco*RV and *Hin*dIII sites of pBR322, to give pILL824. Insertion of the H19 adaptor (carrying an RBS and ATG in frame with *ureE*, Table 1) into a *Bcl*I site overlapping the two first codons of *ureE* in pILL824 produced pILL825 (Figure 2A). The *Bam*HI fragment of pILL825 was then replaced by a 1.3 Kb blunt-ended *Pvu*II-*Bam*HI fragment from pILL753. This resulted in the reconstitution of a complete *ureI* gene, and this plasmid was called pILL833. Finally, pILL834 was obtained by replacement of the *Hpa*I-*Bgl*II fragment of pILL833 (thereby deleting all but the first 21 codons of *ureI*) with an 850 bp blunt-ended *Eco*RI-*Bam*HI fragment of pUC18K2 containing the non-polar Km cassette (19).

TABLE 1:Name and nucleotide sequence of oligonucleotides

Primer	Oligodeoxynucleotide sequence (5' to 3')
H17	TTTGACTTACTGGGGATCAAGCCTG (SEQ ID NO:1)
H19*	GATCATTTATTCCTCCAGATCTGGAGGAATAAAT (SEQ ID NO:2)
H28	GAAGATCTCTAGGACTTGTATTGTTATAT (SEQ ID NO:3)
H34	TATCAACGGTGGTATATCCAGTG (SEQ ID NO:4)
H35	GCAGTTATTGGTGCCCTTAAACG (SEQ ID NO:5)
H50	CCGGTGATATTCTCATTTTAGCC (SEQ ID NO:6)
8A	GCGAGTATGTAGGTTCAGTA (SEQ ID NO:7)
9B	GTGATACTTGAGCAATATCTTCAGC (SEQ ID NO:8)
12B	CAAATCCACATAATCCACGCTGAAATC (SEQ ID NO:9)

*H19 was used as adaptor and the others were used as primers for PCR amplification.

Introduction of *ureI* mutations into *H. pylori*

H. pylori ureI mutants were produced by allelic exchange following electroporation with a concentrated preparation of pILL823 and pILL834 as previously described by

Skouloubris et al. (23) from *H. pylori* strain N6 (12) and from the mouse-adapted *H. pylori* strain, SS1 (Sydney Strain, 17). Bacteria with chromosomal allelic exchange with pILL823 were selected on Cm (4 µg/ml) and those with chromosomal allelic exchange with pILL834 on Km (20 µg/ml). It was determined that the desired allelic exchange had taken place in strains N6-823, N6-834, and SS1-834 (Figure 1) by performing PCR with the appropriate oligonucleotides (Table 1). The PCR products obtained with genomic DNA of these strains were as expected (i) for strain N6-823: 140 bp with primers H28-H34, 220 bp with H35-9B, and 1.2 Kb with H28-9B, and (ii) for strains N6-834 and SS1-834, 150 bp with primers H28-H50, 180 bp with H17-12B, and 1 Kb with H28-12B.

The growth rate of strain N6-834 carrying a non-polar deletion of *ureI* was compared to that of the parental strain N6. No difference in the colony size was observed on blood agar medium plates. Identical doubling times and stationary phase OD were measured for both strains grown in BHI (Oxoid) liquid medium containing 0.2% Ǝ-cyclodextrin (Sigma). Thus, UreI is not essential for *H. pylori* growth *in vitro*.

Urease activity of *H. pylori ureI* mutants

The urease activity of strains N6-823, N6-834, and SS1-834 was measured *in vitro* as described previously by Cussac et al. (9) and compared to the activity of the parental strains, N6 and SS1 (Figure 1). Urease activity was almost completely abolished in strain N6-823 (0.3±0.1 units). Strains N6-834 and SS1-834, with non-polar *ureI* mutations had wild-type levels of activity (N6-834 and SS1-834: 12±2 units; parental strains, N6: 10±1 and SS1: 12±0.4 units).

The pH optimum of urease produced either from the N6 parental strain or from the UreI deficient strain N6-834 was measured and compared. For both strains, urease has a pH optimum of 8 which is consistent with the published data.

These results strongly suggest that the urease-negative phenotype of the N6-*ureI*::TnKm-8 (13) and the very weak urease activity of N6-823 strains were due to a polar effect of the inserted cassettes on the expression of the downstream genes *ureE* and *ureF* (Figure 1). This hypothesis was tested by measuring urease activity of strain N6-823 complemented *in trans* with an *E. coli/H. pylori* shuttle plasmid expressing the *ureE-F* genes. This plasmid, pILL845 (Figure 2B), was obtained by insertion of a 2.8 Kb *Cla*I-

*Bam*HI fragment of pILL834 (comprising the 3'-end of *ureB*, the non-polar deletion of *urel* and intact *ureE* and *ureF* genes) into the corresponding sites of the shuttle vector pHel2 constructed by Heuermann and Haas (15). Strain N6-823 was electroporated with a DNA preparation of pILL845 as described by Skouloubris et al. (23), and transformants were selected on kanamycin (20µg/ml) and chloramphenicol (4µg/ml). In strain N6-823 harboring pILL845, wild type urease activity was recovered confirming that the very low urease activity of strain N6-823 was due to a polar effect on the expression of the accessory genes *ureE-F*. In *Klebsiella aerogenes*, the absence of UreE has little effect on urease activity (4). In contrast. UreF, as part of the accessory protein complex (UreDFG), is absolutely required for the production of active urease (21). Thus, by analogy, it is likely that the phenotype of the *H. pylori* polar *urel* mutants was due to the absence of *ureF* expression.

The urease structural subunits, UreA and UreB, produced by strain N6 or strain N6-834 were compared with the Western blot technique using a mixture of antisera directed against each urease subunit. It was observed that the amount of each subunit produced by the two strains is identical. The possibility that urease cellular localization could be affected in the absence of Urel was examined after cellular fractionation (separating the soluble from the membrane associated proteins and from the supernatant) of strains N6 and N6-834. These experiments revealed no difference between the urease cellular localization in the wild type strain or in the Urel-deficient mutant. These results demonstrate that, at neutral pH, Urel is neither implicated in the stabilization of the urease structural subunits nor in a targeting process of urease to a specific cellular compartment.

Colonization test for the *H. pylori* SS1-834 mutant in the mouse animal model

The mouse model for infection by the *H. pylori* SS1 strain (Sydney Strain, 17), validated by Chevalier et al. (7) and Ferrero et al. (14), was used to test the function of Urel *in vivo*. Mice were infected with the non-polar *urel* mutant, SS1-834, and with the parental strain, SS1, (which had gone through an equivalent number of *in vitro* subcultures) as a positive control. This experiment was repeated three times and produced identical results (30). Two independently constructed SS1-834 mutants were used. The first mutant strain had gone through 30 *in vitro* subcultures, the second only 20. Under the same experimental

conditions, strain SS1 can undergo more than 80 *in vitro* subcultures without losing its colonization capacity.

In each experiment, aliquots (100 µl) containing 10^6 *H. pylori* strain SS1 or SS1-834 bacteria prepared in peptone broth were administered orogastrically to 10 mice each (six to eight-weeks old Swiss specific-pathogen-free mice) as described by Ferrero et al. (14). Mice were killed four weeks after inoculation. The presence of *H. pylori* was tested with a direct urease test on biopsies performed on half the stomach (14). The remaining gastric tissues were used for quantitative culture of *H. pylori* as described by Ferrero *et al.* (14). In each experiment, the stomachs of the ten SS1-infected mice all tested positive for urease. The bacterial load was between $5x10^4$ and $5x10^5$ colony forming units (CFU) per g of stomach. None of the stomachs of the mice infected with strain SS1-834 tested positive for urease and no *H. pylori* cells were cultured from them. Thus, the UreI protein is essential for the *H. pylori in vivo* survival and/or colonization of the mouse stomach.

UreI is essential for *H. pylori* resistance to acidity

Survival to acidic conditions in the presence or absence of 10mM urea was tested with strains N6 and N6-834. The experimental procedures detailed in Skouloubris *et al.* (30) were based on those described in Clyne *et al.* (8). Exponentially grown bacteria were harvested, washed in PBS (phosphate buffer saline), and approximately 2 $X10^8$ CFU/ml were resuspended in PBS of pH 2.2 or pH 7 in the presence or the absence of 10mM urea and incubated at 37EC. After one hour incubation (i) quantitative cultures of the *H. pylori* strains were performed to evaluate bacterial survival, and (ii) the bacteria were centrifuged and the pH of the medium was measured. The results obtained are presented in Table 2. In the absence of urea, both strains N6 and N6-834 presented identical phenotype, i.e., they were killed at pH 2.2, and survived at pH 7 without modifying the final pH of the medium (Table 2). After incubation at pH 7 in the presence of urea, both strains were killed because the final pH rose to pH 9. At pH 2.2 in the presence of urea, the parental strain survived well since it was able to raise the pH to neutrality. In contrast, a completely different phenotype was obtained with the UreI-deficient strain N6-834 which was unable to raise the pH and whose viability was seriously affected (Table 2).

Complementation of the UreI-deficient strain N6-834 with plasmid pILL850

Direct implication of the UreI protein in the *H. pylori* capacity to resist to acidity has been confirmed by trans-complementation with plasmid pILL850 (Figure 2B restriction map and details of construction). This plasmid [CNCM I-2245 filed on June 28,1999] is derived from the *H. pylori/E. coli* shuttle vector pHel2 (15). Plasmid pILL850 carries the *ureI* gene under the control of its own promoter and was constructed as follows: a 1.2 kb *BclI* restriction fragment of plasmid pILL753 (9) was introduced between the *Bam*HI and *BclI* restriction sites of pHel2 (Figure 2B). Strains N6 and N6-834 were transformed by this plasmid and the phenotype of the complemented strains in the acidity sensitivity test experiments described above was examined. As shown in Table 2, the phenotype of strain N6-834 complemented by pILL850 is identical to that of the parental strain N6. Interestingly, the urease activity of the complemented strains (measured on sonicated extracts as described in Skouloubris *et al.* (30)) has been found to be significantly higher as compared to that of the corresponding strains without pILL850. For the purpose of the deposit at the CNCM pILL850 is placed into an E. coli strain, MC1061 (Wertman KF. et al, 1986, Gene 49: 253-262).

Measurements of ammonium production

The amount of ammonium produced in the extracellular medium of *H. pylori* whole cells was measured by an enzymatic assay commercialized by Sigma following the supplier's instructions. These experiments were performed after incubation of the cells in PBS at different pH values and after different incubation times. Such experiments gave an accurate evaluation of ammonium production and excretion in different strains as well as a measure of the kinetics of this reaction. A control experiment showed that ammonium production was very low (10-20µM) in the absence of urea.

Figure 4 depicts the kinetics (0, 3, 5, and 30 min. incubation time) of extracellular ammonium released by the N6 parental strain (panel A) and the UreI-deficient strain N6-834 (panel B) incubated in PBS at pH 2.2, pH 5, or pH 7 in the presence of 10mM urea. The results obtained indicate that (i) ammonium is largely produced and rapidly released in the extracellular medium; and (ii) in the N6 wild type strain (Figure 4, panel A and Table 3) ammonium production is significantly enhanced when the extracellular pH is acidic. This effect is already visible at pH 5 and is even stronger at pH 2.2. This last observation is

consistent with the results of Scott *et al.* (31) who suggested urease activation at low pH. In our experiments, the rapidity of the response to acidity argues against urease activation depending on transcriptional regulation or on *de novo* protein synthesis.

Ammonium production was then measured in the UreI-deficient strain N6-834 (Figure 4, panel B and Table 3). At neutral pH, kinetics of ammonium production were similar to those of the wild type strain. In contrast, at pH 5 ammonium production was reduced and delayed as compared to the wild type strain. A dramatic effect of the absence of UreI was observed at pH 2.2, where the amount of ammonium was very low, which is consistent with our results showing that UreI is necessary for adaptation to acidity.

Our results demonstrate that UreI is essential for the resistance of *H. pylori* to acidity. In the absence of UreI. urease, although present in huge amounts, is not able to protect the bacteria against the aggression of acidity. This is consistent with the essential role of UreI *in vivo*. During its passage in the acidic stomach lumen, the viability of the UreI-deficient strain is affected. As a consequence, the bacterial load becomes too low to permit colonization. The different roles proposed for UreI are presented in the "detailed description" section.

Alignment of the UreI and AmiS protein sequences and two dimensional structure prediction

A systematic search for UreI homologs in the protein data banks was carried out. It was determined that *H. pylori* is not the only ureolytic bacterium with a *urel* gene. Two phylogenetically related Gram-positive organisms, *Streptococcus salivarius*, a dental plaque bacterium (6), and *Lactobacillus fermentum*, a lactic acid bacterium (16), carry genes for UreI-homologs (Figure 3) located immediately upstream from the urease structural genes. The *urel* gene has been detected in various *Helicobacter* species; the *H. felis urel* gene has been entirely sequenced (Figure 3 and allowed United Stated Patent application Serial No. 08/467,822, the entire contents of which are incorporated herein by reference). PCR experiments have suggested that there is a *urel* gene in *H. heilmannii* (24) and in *H. mustelae*.

Sequence similarities between the UreI protein of *H. pylori* and the AmiS proteins expressed by the aliphatic amidase operons from *P. aeruginosa* (27) and *Rhodococcus* sp.

R312 (5) have been reported. In *Mycobacterium smegmatis*, there is an additional AmiS-homolog encoded by a gene, ORF P3, located immediately upstream from an amidase gene (18).

Alignment of these UreI/AmiS proteins [using the Clustal W(1. 60) program] defined strongly conserved stretches of amino acids (Figure 3). All but one of these conserved blocks are in highly hydrophobic segments. These regions, each 17 to 22 residues long, are probably folded into transmembrane ∀-helices (Figure 3). Six transmembrane regions were predicted for the proteins from *H. pylori*, *H. felis*, and *P. aeruginosa* and seven for those from *Rhodococcus* sp. R312 and *M. smegmatis* (highly reliable predictions, performed with pHD, a profile fed neural network system as described by Rost et al. (22)). The orientation of the UreI/AmiS proteins in the membrane was deduced from the charges of the intercalated hydrophilic regions, which are short in these proteins (Figure 3). The first five such regions are poorly conserved and of various length. The last interhelical segment common to these proteins is significantly more conserved than the others. This region predicted to be intracellular may be the active site of UreI or a site of multimerization or interaction with an intracellular partner. These results strongly suggest that the members of the UreI/AmiS family, found in both Gram-positive and -negative bacteria, are integral membrane proteins. These proteins have no signal sequence and should therefore be inserted into the cytoplasmic membrane in Gram-negative bacteria.

Two peptides, selected from the UreI sequence, were synthesized and injected into two rabbits to obtain serum containing polyclonal antibodies directed against UreI. One peptide corresponds to the first predicted intracellular loop of UreI (from residue nB 15 to 31, see Figure 3) and the second one to the second predicted extracellular loop of UreI (from residue nB 118 to 134, see Figure 3. These sera are presently being tested and if proven to recognize the UreI protein will allow us to precisely define the localization of this protein and to verify the predicted UreI two-dimensional structure presented in Figure 3.

The references cited herein are specifically incorporated by reference in their entirety.

strains	initial pH	final pH	urea 10mM	*H. pylori* CFU/ml
N6	2.2	2.26	-	0
N6	2.2	6.6	+	$8x10^7$
N6	7	6.98	-	$2x10^8$
N6	7	8.88	+	0
N6-834	2.2	2.2	-	0
N6-834	2.2	2.37	+	$7x10^5$
N6-834	7	7.1	-	$3.5x10^7$
N6-834	7	9.05	+	0
N6-834+pILL850	2.2	2.3	-	0
N6-834+pILL850	2.2	6.9	+	$1.3x10^8$
N6-834+pILL850	7	7.1	-	$1.7x10^8$
N6-834+pILL850	7	9	+	0

Table 2 : Effect of the presence of urea at pH 7, 5 or 2.2 on (i) the viability of different *H. pylori* strains and (ii) the extracellular pH (indicated as final pH). The experimental procedures are described in reference 30 and in the examples. Strain N6 is the parental strain and strain N6-834 the UreI-deficient mutant. Plasmid pILL850 is derived from a *E. coli/H. pylori* shuttle vector, it carries the *ureI* gene and complements the *ureI* mutation of strain N6-834.

Table 3

Strain	medium pH	minutes	[NH4] mM
N6	7,0	0	3.5
N6	7,0	3	4.4
N6	7,0	5	3.1
N6	7,0	30	5.6
N6	5,0	0	12.8
N6	5,0	3	9.3
N6	5,0	5	11.8
N6	5,0	30	16,0
N6	2,2	0	6.7
N6	2,2	3	9,0
N6	2,2	5	11,0
N6	2,2	30	20,0
N6-834	7,0	0	2,.7
N6-834	7,0	3	2.8
N6-834	7,0	5	3.8
N6-834	7,0	30	5.8
N6-834	5,0	0	1.4
N6-834	5,0	3	1.7
N6-834	5,0	5	2.9
N6-834	5,0	30	4.6
N6-834	2,2	0	0.9
N6-834	2,2	3	0.6
N6-834	2,2	5	0.7
N6-834	2,2	30	1.3

REFERENCES

1. **Akada, J. K., M. Shirai, H. Takeuchi, M. Tsuda, and T. Nakazawa.** 1997. Transcriptional analysis of urease structural gene and the *urel* gene in *Helicobacter pylori*. Gut. **41**:A9.

2. **Allaoui, A., Schulte, R. and G. R. Cornelis.** 1995. Mutational analysis of the *Yersinia enterocolitica virC* operon: characterization of *yscE, F, G, H, I, J, K* required for Yop secretion and *ysch* encoding YopR. Mol. Microbiol. **18**:343-355.

3. **Bauerfeind, P., R. M. Garner, and H. L. T. Mobley.** 1996. Allelic exchange mutagenesis of *nixA* in *Helicobacter pylori* results in reduced nickel transport and urease activity. Infect. Immun. **64**:2877-2880.

4. **Brayman, T. G., and R. T. Hausinger.** 1996. Purification, characterization, and functional analysis of a truncated *Klebsiella aerogenes* UreE urease accessory protein lacking the Histidine-Rich carboxyl terminus. J. Bacteriol. **178**:5410-5416.

5. **Chebrou, H., F. Bigey, A. Arnaud, and P. Galzy.** 1996. Amide metabolism: a putative ABC transporter in *Rhodococcus* sp. R312. Gene. **182**:215-218.

6. **Chen, Y.-Y. M., K. A. Clancy, and R. A. Burne.** 1996. *Streptococcus salivarius* urease: genetic and biochemical characterization and expression in a dental plaque Streptococcus. Infect. Immun. **64**:585-592.

7. **Chevalier, C., J.-M. Thiberge, R. L. Ferrero, and A. Labigne.** 1999. Essential role of *Helicobacter pylori* g-Glutamyltranspeptidase (GGT) for the colonization of the gastric mucosa in mice. Mol. Microbiol. **31**:1359-1372.

8. **Clyne, M., A. Labigne, and B. Drumm.** 1995. *Helicobacter pylori* requires an acidic environment to survive in the presence of urea. Infect. Immun. **63**:1669-1673.

9. **Cussac, V., R. L. Ferrero, and A. Labigne.** 1992. Expression of *Helicobacter pylori* urease genes in *Escherichia coli* grown under nitrogen-limiting conditions. J. Bacteriol. **174**:2466-2473.

10. **Dunn, B. E., H. Cohen, and M. Blaser.** 1997. *Helicobacter pylori*. Clin. Microbiol. Rev. **10**:720-741.

11. **Eaton, K. A., and S. Krakowka.** 1994. Effect of gastric pH on urease-dependent colonization of gnotobiotic piglets by *Helicobacter pylori*. Infect. Immun. **62**:3604-3607.

12. **Ferrero, R. L., V. Cussac, P. Courcoux, and A. Labigne.** 1992. Construction of isogenic urease-negative mutants of *Helicobacter pylori* by allelic exchange. J. Bacteriol. **174**:4212-4217.

13. **Ferrero, R. L., V. Cussac, P. Courcoux, and A. Labigne.** 1994. Construction of isogenic mutants of *Helicobacter pylori* deficient in urease activity. pp179-182. *In* Basic and Clinical Aspects of *H. pylori* infection. Springer-Verlag Berlin Heidelberg.

14. **Ferrero, R. L., J.-M. Thiberge, M. Huerre, and A. Labigne.** 1998. Immune responses of specific-pathogen-free mice to chronic *Helicobacter pylori* (strain SS1) infection. Infect. Immun. **66**:1349-1355.

15. **Heuermann, D., and R. Haas.** 1998. A stable shuttle vector system for efficient genetic complementation of *Helicobacter pylori* strains by complementation and conjugation. Mol. Gen. Genet. **257**:519-528.

16. **Kakimoto, S., Y. Sumino, K. Kawahara, E. Yamazaki, and I. Nakatsui.** 1990. Purification and characterization of acid urease from *Lactobacillus fermentum*. Appl. Microbiol. & Biotechnol. **32**:538-543.

17. **Lee, A., J. O'Rourke, M. Corazon De Ungria, B. Robertson, G. Daskalopoulos, and M. F. Dixon.** 1997. A standardized mouse model of *Helicobacter pylori* infection: introducing the Sydney Strain. Gastroenterology. **112:**1386-1397.

18. **Mahenthiralingam, E., P. Draper, E. O. Davis, and M. J. Colston.** 1993. Cloning and sequencing of the gene which encodes the highly inducible acetamidase of *Mycobacterium smegmatis*. J. Gen. Microbiol. **139:**575-583.

19. **Menard, R., P. J. Sansonetti, and C. Parsot.** 1993. Nonpolar mutagenesis of the *ipa* genes defines IpaB, IpaC, and IpaD as effectors of *Shigella flexneri* entry into epithelial cells. J. Bacteriol. **175:**5899-5906.

20. **Mobley, H. L. T., M. D. Island, and R. P. Hausinger.** 1995. Molecular biology of ureases. Microbiol. Rev. **59:**451-480.

21. **Moncrief, M. B. C., and R. P. Hausinger.** 1997. Characterization of UreG, identification of a UreD-UreF-UreG complex, and evidence suggesting that a nucleotide-binding site in UreG is required for *in vivo* metallocenter assembly of *Klebsiella aerogenes* urease. J. Bacteriol. **179:**4081-4086.

22. **Rost, B., R. Casadio, P. Fariselli, and C. Sander.** 1995. Prediction of helical transmembrane segments at 95% accuracy. Prot. Science. **4:**521-533.

23. **Skouloubris, S., A. Labigne, and H. De Reuse.** 1997. Identification and characterization of an aliphatic amidase in *Helicobacter pylori*. Mol. Microbiol. **25:**989-998.

24. **Solnick, J. V., J. O'Rourke, A. Lee, and L. S. Tompkins.** 1994. Molecular analysis of urease genes from a newly identified uncultured species of *Helicobacter*. Infect. Immun. **62:**1631-1638.

25. **Trieu-Cuot, P., G. Gerbaud, T. Lambert, and P. Courvalin.** 1985. *In vivo* transfer of genetic information between Gram-positive and Gram-negative bacteria. EMBO J. 4:3583-3587.

26. **Williams, C. L., T. Preston, M. Hossack, C. Slater, and K. E. L. McColl.** 1996. *Helicobacter pylori* utilizes urea for amino acid synthesis. FEMS Immunol. Med. Microbiol. **13**:87-94.

27. **Wilson, S. A., R. J. Williams, L. H. Pearl, and R. E. Drew.** 1995. Identification of two new genes in the *Pseudomonas aeruginosa* amidase operon, encoding an ATPase (AmiB) and a putative integral membrane protein (AmiS). J. Biol. Chem. **270**:18818-18824.

28. **Mendz, G.L. and S.L. Mazell.** 1996. The Urea Cycle of *Helicobacter pylori*. Microbiology 142:2959-2967.

29. **Nicholson, E.B., E.A. Concaugh and H.L.T. Mobley**. 1991. *Proteus mirabilis* urease: use of ureA-lacZ fusion demonstrates that induction is highly specific for urea. Infection and Immunity. 59(10):3360-3365.

30. **Skouloubris, S., J.-M. Thiberge, A. Labigne and H. De Reuse** (1998) The *Helicobacter pylori* UreI protein is not involved in urease activity but is essential for bacterial survival *in vivo*. Infect. Immun. **66**: 4517-4521.

31. **Scott, D. R., D. Weeks, C. Hong, S. Postius, K. Melchers and G. Sachs** (1998) The role of internal urease in acid resistance of *Helicobacter pylori*. Gastroenterology. 114: 58-70.